

1 GGCACGAGGT CCCCACGCG CCCC GCCAA CCCCTACGAT GAAGAGGGCG 50
 1 M K R A 4
 51 TCCGCTGGAG GGAGCCGGCT GCTGGCATGG GTGCTGTGGC TGCAGGCCTG 100
 5 S A G G S R L L A W V L W L Q A W 21
 101 GCAGGTGGCA GCGCCATGCC CAGGTGCCTG CGTATGCTAC AATGAGCCCA 150
 22 Q V A A P C P G A C V C Y N E P K 38
 151 AGGTGACGAC AAGCTGCCCC CAGCAGGGCC TGCAGGCTGT GCCCGTGGGC 200
 39 V T T S C P Q Q G L Q A V P V G 54
 201 ATCCCTGCTG CCAGCCAGCG CATCTTCCTG CACGGCAACC GCATCTCGCA 250
 55 I P A A S Q R I F L H G N R I S H 71
 251 TGTGCCAGCT GCCAGCTTCC GTGCCTGCCG CAACCTCACC ATCCTGTGGC 300
 72 V P A A S F R A C R N L T I L W L 88
 301 TGCACTCGAA TGTGCTGGCC CGAATTGATG CGGCTGCCTT CACTGGCCTG 350
 89 H S N V L A R I D A A A F T G L 104
 351 GCCCTCCTGG AGCAGCTGGA CCTCAGCGAT AATGCACAGC TCCGGTCTGT 400
 105 A L L E Q L D L S D N A Q L R S V 121
 401 GGACCCTGCC ACATTCCACG GCCTGGGCGG CCTACACACG CTGCACCTGG 450
 122 D P A T F H G L G R L H T L H L D 138
 451 ACCGCTGCGG CCTGCAGGAG CTGGGCGCGG GGCTGTTCCG CGGCCTGGCT 500
 139 R C G L Q E L G P G L F R G L A 154
 501 GCCCTGCAGT ACCTCTACCT GCAGGACAAC GCGCTGCAGG CACTGCCTGA 550
 155 A L Q Y L Y L Q D N A L Q A L P D 171
 551 TGACACCTTC CGCGACCTGG GCAACCTCAC ACACCTCTTC CTGCACGGCA 600
 172 D T F R D L G N L T H L F L H G N 188

FIG. 1A

601 ACCGCATCTC CAGCGTGCCC GAGCGCGCCT TCCGTGGGCT GCACAGCCTC 650
 189 R I S S V P E R A F R G L H S L 204
 651 GACCGTCTCC TACTGCACCA GAACCGCGTG GCCCATGTGC ACCCGCATGC 700
 205 D R L L L H Q N R V A H V H P H A 221
 701 CTTCCGTGAC CTTGGCCGCC TCATGACACT CTATCTGTTT GCCAACAATC 750
 222 F R D L G R L M T L Y L F A N N L 238
 751 TATCAGCGCT GCCCACTGAG GCCCTGGCCC CCCTGCGTGC CCTGCAGTAC 800
 239 S A L P T E A L A P L R A L Q Y 254
 801 CTGAGGCTCA ACGACAACCC CTGGGTGTGT GACTGCCGGG CACGCCCCACT 850
 255 L R L N D N P W V C D C R A R P L 271
 851 CTGGGCCTGG CTGCAGAAGT TCCGCGGCTC CTCCTCCGAG GTGCCCTGCA 900
 272 W A W L Q K F R G S S S E V P C S 288
 901 GCCTCCCGCA ACGCCTGGCT GGCCGTGACC TCAAACGCCT AGCTGCCAAT 950
 289 L P Q R L A G R D L K R L A A N 304
 951 GACCTGCAGG GCTGCGCTGT GGCCACCGGC CCTTACCATC CCATCTGGAC 1000
 305 D L Q G C A V A T G P Y H P I W T 321
 1001 CGGCAGGGCC ACCGATGAGG AGCCGCTGGG GCTTCCCAAG TGCTGCCAGC 1050
 322 G R A T D E E P L G L P K C C Q P 338
 1051 CAGATGCCGC TGACAAGGCC TCAGTACTGG AGCCTGGAAG ACCAGCTTCG 1100
 339 D A A D K A S V L E P G R P A S 354
 1101 GCAGGCAATG CGCTGAAGGG ACGCGTGCCG CCCGGTGACA GCCCGCCGGG 1150
 355 A G N A L K G R V P P G D S P P G 371
 1151 CAACGGCTCT GGGCCACGGC ACATCAATGA CTCACCCTTT GGGACTCTGC 1200
 372 N G S G P R H I N D S P F G T L P 388

FIG. 1B

1201 CTGGCTCTGC TGAGCCCCCG GCTCACTGCA GTGCGGCCCCG AGGGCTCCGA 1250
 389 G S A E P P A H C S A A R G L R 404
 1251 GCCACCAGGT TCCCCACTTC GGGCCCTCGC CGGAGGCCAG GCTGTTACAG 1300
 405 A T R F P T S G P R R R P G C S R 421
 1301 CAAGAACCGC ACCCGCAGCC ACTGCCGTCT GGGCCAGGCA GGCAGCGGGG 1350
 422 K N R T R S H C R L G Q A G S G G 438
 1351 GTGGCGGGAC TGGTGACTCA GAAGGCTCAG GTGCCCTACC CAGCCTCACC 1400
 439 G G T G D S E G S G A L P S L T 454
 1401 TGCAGCCTCA CCCCCCTGGG CCTGGCGCTG GTGCTGTGGA CAGTGCTTGG 1450
 455 C S L T P L G L A L V L W T V L G 471
 1451 GCCCTGCTGA CCCCCAGCGG ACACAAGAGC GTGCTCAGCA GCCAGGTGTG 1500
 472 P C * 473
 1501 TGTACATACG GGGTCTCTCT CCACGCCGCC AAGCCAGCCG GGCGGCCGAC 1550
 1551 CCGTGGGGCA GGCCAGGCCA GGTCCCTCCCT GATGGACGCC TGCCGCCCCG 1600
 1601 CACCCCCATC TCCACCCCAT CATGTTTACA GGGTTCGGCG GCAGCGTTTG 1650
 1651 TTCCAGAACG CCGCCTCCCA CCCAGATCGC GGTATATAGA GATATGCATT 1700
 1701 TTATTTTACT TGTGTAAAAA TATCGGACGA CGTGGAATAA AGAGCTCTTT 1750
 1751 TCTTAAAAAA AAAAAAAAAA AACTCGA 1777

FIG. 1C

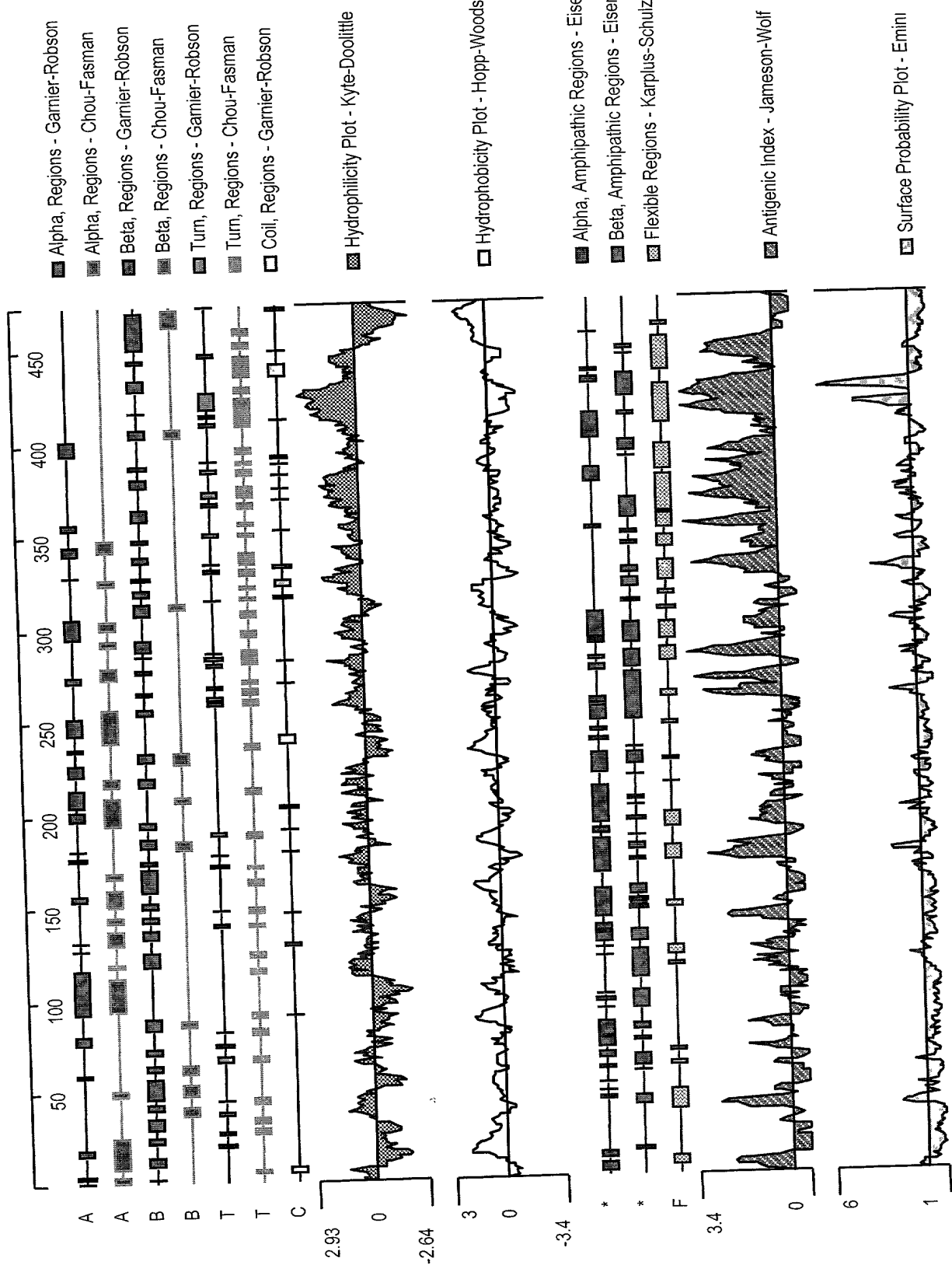


FIG. 2